

Looking for the vector of the latest discovered geminivirus genus, *Capulavirus*

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Viral metagenomics studies based on virion-associated nucleic acid extraction, sequence-independent amplification and next generation sequencing proved to be effective for discovering three highly divergent geminiviruses in South Africa, France and Finland. Although these geminiviral sequences were isolated from different continents, hemispheres and plant families, including *Euphorbia caput-medusae* (*Euphorbiaceae*), *Medicago sativa* (*Fabaceae*) and *Plantago lanceolata* (*Plantaginaceae*), they were clustered in the same phylogenetic group and were highly divergent from all the sequences classified in the seven established geminivirus genera. Based on sequence relatedness and genome organization, these new highly divergent geminivirus species were provisionally classified in a new geminivirus genus, tentatively named “Capulavirus”.

To estimate the epidemiological potential of these new geminiviruses but also to confirm their classification according to the criteria defined by the International Committee on Taxonomy of Viruses, including insect vector and host range, further studies were done with two capulaviruses available in our laboratory: *Euphorbia caput medusae* latent virus (EcmLV) from South Africa (Bernardo et al. 2013) and a capulavirus isolated from alfalfa in France provisionally named Alfalfa leaf curl virus (ALCV) according to the symptoms observed on infected plants. ALCV may cause yield losses because the infected plants exhibited stunting and distorted growth. ALCV was detected in Camargue, Provence Alpes Côte d’Azur, Languedoc Roussillon and Midi-Pyrénées.

An infectious clone of EcmLV was prepared and used to determine the host range of EcmLV and test various phloem feeding insects reared in our laboratory, for vector transmission. Potentially infectious clones are presently prepared for ALCV for similar tests. In the meantime, a naturally infected alfalfa plant was transferred to a growth chamber and used as source plant for vector transmission. Potential vectors were also collected from infected alfalfa fields for testing ALCV transmission to alfalfa seedlings prepared in insect proof conditions.

Mots-clés : Transmission, alfalfa, insect, metagenomics.